Determination of the Prevalence of Helicobacter bilis by PCR in Iranian Mus Musculuse

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Background & Objectives: Infectious diseases of of free-living wild mus have the potential of carrying zoonosis Diseases, *Helicobacter bilis* is member of the murine enterohepatic Helicobacter spp., Since discovery Helicobacter bilis from bile, liver, and intestine of aged, inbred mice and associated with liver and hepatobiliary tract disease in human patients. The aim of this study is planned the molecular study to investigate To determine whether presence of Helicobacter species, particularly *Helicobacter bilisin* liver of Mus musculuse from six interurban's areas of Isfahan province (Isfahan, Najafabad, Fereydunshahr, Mobarakeh, Golpayegan and Kashan), and evalouatin of molecular frecuensy of this bacterium in mus musculuse in this region.

Methods: 300 wild mice were collected withlive traps and glue traps, Liver specimens were removed and collected aseptically at necropsy immediately after euthanasia the mice by inhalation of CO2 within 24 h of entrapment in CO_2 chamber. DNA was extracted from specimen using the DNA extraction kit and Nested PCR was performed on template DNA.

Results: From 300 liver samples which asseyd, 204 (68%) samples were positive for genus Helicobacter and 118 (39.33%) samples were positive for *Helicobacter bilis* ($P \leq 0.05$).

Conclusion: In conclusion, PCR technique can detect *H. bilis* DNA in liver samples of Mus musculuse in center of Iran. To the best of our knowledge, this is the first report on the detection of H. bilis on Mus musculuse liver in Isfahan provenis, Iran. In our opinion One of the possibilities is that samples not identified to the species level by PCR may represent other possible hepatobiliary Helicobacter species, such as H. hepaticus and the more recently discovered *Helicobacter rodentium* and *H. mastomyrinus* are one possible explanation.

Keywords: *Helicobacter bilis*; Nested-PCR; Mus Musculuse